underlining. A clean version of the pending claims, as amended, is attached hereto as Exhibit B.

Please amend the claims as follows:

Cancel claims 2-3, 35, 182, 214-262 and 268-279, without prejudice.

Amend claims 1, 4-6, 11-12, 30, 36, 89-90, 158-159, 177, 183, and 263-264 to read as follows:

1. (Amended) A method for analyzing exon expression in a cell sample, comprising measuring the expression levels of a plurality of different individual exons or different individual multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, wherein at least one gene in said plurality of different genes comprises an exon possibly having a plurality of different variants, each of said plurality of different variants being a form of said exon generated using a different splice junction of said exon, and wherein the measured expression levels of said different individual exons or different individual multiexons in said gene are sufficient for determining which of said plurality of different variants of said exon is, and which is not, expressed in said cell sample, and determining which of said plurality of different variants of said exon is, and which is not, expressed; thereby analyzing the exon expression of said cell sample.

4. (Amended) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons or multiexons.

5. (Amended) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons or multiexons.

6. (Amended) The method of claim 1, wherein said plurality of different individual exons or different individual multiexons consists of at least two different exons.

11. (Amended) The method of claim 10, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons.

12. (Amended) The method of claim 10, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons.

30. (Amended) The method of claim 10, wherein at least one of said plurality of

polynucleotide probes comprises a nucleotide sequence complementary to the sequence of a full length exon.

36. (Amended) The method of claim 1 or 10, wherein said expression levels are measured as absolute abundance.

89. (Amended) The method of claim 86, further comprising comparing the expression levels of at least a portion of said plurality of different individual exons or different individual multiexons in said cell sample having been subjected to said perturbation with the expression level of said portion of said plurality of different individual exons or different individual multiexons in a cell sample of the same type not having been subjected to said perturbation.

90. (Amended) The method of claim 89, wherein said comparing comprises determining the difference between the expression level of each exon or multiexon in said portion of said plurality of different individual exons or different individual multiexons in said cell sample having been subjected to said perturbation and the expression level of the corresponding exons or multiexons in said cell sample of the same type not having been subjected to said perturbation.

158. (Amended) The method of claim 157, wherein said plurality of different individual exons or different individual multiexons consists of at least 3 different exons.

159. (Amended) The method of claim 157, wherein said plurality of different individual exons or different individual multiexons consists of at least 5 different exons.

177. (Amended) The method of claim 157, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary to the sequence of a full length exon.

183. (Amended) The method of claim 157, wherein said expression levels are measured as absolute abundance.

263. (Amended) The method of claim 10 or 157, wherein said array of polynucleotide probes comprises one or more sets of successive overlapping probes tiled

along the longest variant of said exon having a plurality of different variants.

264. (Amended) The method of claim 10 or 157, wherein said array of polynucleotide probes comprises variant junction probes, wherein each of said variant junction probes is specifically hybridizable to a sequence spanning the splice junction between a different variant of said exon having a plurality of different variants and a neighboring exon.

Add new claims as follows:

280. (New) The method of claim 32 or 179, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

281. (New) The method of claim 280, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

282. (New) The method of claim 281, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

283. (New) The method of claim 282, wherein each of said different nucleotide sequences consists of 60 nucleotides.

284. (New) A method for analyzing exon expression in a cell sample of an organism, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises (i) one or more exon specific probes of different nucleotide sequences for each of a plurality of different genes in the genome of said organism, each of said different nucleotide sequences being complementary and hybridizable to a sequence within a different individual exon; and (ii) a variant junction probe for each of a plurality of different possible variants of at least one exon, each of said variants being a form of said exon generated using a different splice junction

of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and a neighboring exon in a multiexon comprising said variant of said exon, each of said exon specific probes and variant junction probes being bound to a different region of a support; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

285. (New) A method for analyzing exon expression in a cell sample of an organism, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of junction specific probes of different nucleotide sequences for each of a plurality of different genes in the genome of said organism bound to different regions of a support, each of said different nucleotide sequences being complementary and hybridizable to a sequence spanning a junction region of a multiexon, and wherein said plurality of junction specific probes comprises a variant junction probe for each of a plurality of different possible variants of at least one exon, each of said variants being a form of said exon generated using a different splice junction of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and a neighboring exon in a multiexon comprising said variant of said exon; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

286. (New) The method of claim 284 or 285, wherein said plurality of different genes consists of at least 100 different genes.

287. (New) The method of claim 286, wherein said plurality of different genes consists of at least 1,000 different genes.

288. (New) The method of claim 287, wherein said plurality of different genes consists of at least 10,000 different genes.